### 10/789536

FILE 'REGISTRY' ENTERED AT 12:10:19 ON 21 JAN 2005
L1 157 S GGGGTCAACGTTCAGGGGGG | GCATGACGTTGAGCT/SQSN

FILE 'CAPLUS' ENTERED AT 12:12:01 ON 21 JAN 2005

L2 55 S L1

L8 21 SEA ABB=ON PLU=ON L2(L)(IMMUNOMODULAT? OR IMMUNOSTIMULAT? OR IMMUNOSTIMULAT OR IMMUNORESPONS? OR (IMMUN# OR IMMUNOL?)(3A)(M ODULAT? OR STIMULAT? OR STIMULANT OR RESPONS?))

E1 THROUGH E29 ASSIGNED

Searcher : Shears 571-272-2528

```
Regult
No.
                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                              Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                          Score
    GenEmbl:*
1: gb ba:*
2: gb ht;
3: gb ht;
4: gb om:*
6: gb ov:
6: gb ov:
6: gb ph;
9: gb pl;
9: gb pl;
11: gb gt;
12: gb gt;
13: gb gt;
14: gb gt
                                                                                                                                                                                         Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gapop 10.0 , Gapext 1.0
    January 19, 2005, 01:27:37; Search time 588 Seconds (without alignments) 1608.493 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-789-536-1
20
1 9999tcaac9ttcag9g9g9 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4526729 seqs, 23644849745 residues
                                                                                                                                                                                                                                                                          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
  თთთთთთთთთთთთთთთთ
 AR09668
AR135030
AX342378
AX342378
AX342405
AX342405
AX342405
AX342408
AR1140453
AR1154761
BD15017
BD15017
AR182880
AR182887
AR18437
AR18437
AR18437
AR18437
AR18437
AR18437
                                                                                                                                                                                          Ħ
                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9053458
AR096686 Sequence
AR135030 Sequence
AX342378 Sequence
AX342405 Sequence
AX342405 Sequence
AR140453 Sequence
AR154761 Sequence
BD190419 Microemul
BD251267 Enhanceme
AR182887 Sequence
AR182887 Sequence
AR182887 Sequence
AR432435 Sequence
AX063578 Sequence
AX104375 Sequence
AX104375 Sequence
AX104776 Sequence
AX104777 Sequence
                                                                                                                                                                                        Description
```

ი																									
5	44	43	42	41	40	39	38	37	36	35	34	33	32	μ	30	29	28	27	26	25	24	23	22	21	20
17.4	17.4	•	٠	٠	٠	17.4	٠			•	18.4	8	18.4	18.4		æ	8	æ	18.4	æ	œ	18.4	œ	18.4	18.4
87.0	٠	87.0	87.0	87.0	•	•	•	92.0	•	•	•	•	92.0	•	•	•	•	•	•	٠	92.0	٠	٠	٠	92.0
58145	19	19		19	19	19	24	24	21	21	21	20	20	20	20	20	20	20	20	20	20	20	20	20	20
N	σ	6	σ	σ	σ	σ	σ	σ	σ	φ	σ	6	σ	σ	σ	σ	σ	σ	0	σ	σ	ò	σ	σ	σ
AC013515		AX771751	AX465396	AX194446	CQ753473	CQ753472	AX547379	AX104326	AX547865	AX105257	AX104812	BD069974	BD009060	AX547830	AX547829	AX547628	AX547380	AX468483	AX465439	AX355409	AX355408	AX194489	AX135634	AX105236	AX105103
3515		751	σ	444	3473	CQ753472	AX547379	AX104326	տ				BD009060		9	47628	7380	AX468483	9	5409	œ	4489	34	σ	AX105103
Homo sapi	Sequence	Sequence	Sequence	Sequence	Sequence	ຜ	ശ	Sequence	Sequence	Sequence	Sequence	Use of nu	Immunosti	Sequence											

RESULT 2 AR115030 LOCUS DEPINITION ACCESSION VERSION KEYWOODS SOURCE ORGANISM REFERENCE AUTHORS TITLE	Query Match Best Local Matches 2 Qy 1 Db 1	RESULT 1 AR096686 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES SOUICE ORIGIN
AR135030 20 bp DNA linear Sequence 1 from patent US 6194388. AR135030 GI:14123935 Unknown. Unknown. Unclassified. 1 (Dases 1 to 20) Krieg, A.M., Klinman, D. and Steinberg, A.D. Immunomodulatory oligonucleotides	Query Match 100.0%; Score 20; DB 6; Length 20; Best Local Similarity 100.0%; Pred. No. 19; Matches 20; Conservative 0; Mismatches 0; Indels 1 GGGGTCAACGTTCAGGGGGG 20	AR096686 Sequence 1 from patent US 6008200. AR096686 AR096686.1 GI:10025701 Unknown. Unknown. Unclassified. 1 (bases 1 to 20) Krieg.A.M. Immunomodulatory oligonucleotides Patent: US 6008200-A 1 28-DEC-1999; Location/Qualifiers 1. 20 /organism="unknown" /mol_type="unassigned DNA"
PAT	0,	PAT
16-MAY-2001	Gaps 0;	08-SEP-2000

```
Minimum
Maximum
                                                                                                                                                                            Database
                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Run
                                                                                                                                                                                                                                                                                                                                                                                                                     Title:
Perfect score:
                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OM nucleic -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92
                                                                                                                                                                                                                                                              DB DB
                                                                                                                                                                                                                                                            seq length:
seq length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic search, using sw model
  10:
11:
12:
                                                                                                                                                                                                                                                                                                                                                            IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-789-536-1
20
                                                                                                                                                                                                                                                                                                                                4134886 seqs, 2624710521 residues
                                                                                                                                                          N_Geneseq_23Sep04:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           January 19, 2005, 01:18:22 ;
geneseqn2003as:*
geneseqn2003bs:*
: geneseqn2003cs:*
: geneseqn2003ds:*
: geneseqn2004s:*
                                                                                                                                                                                                                                                                                                                                                                                                     9999tcaacgttcagggggg 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copyright
                                                                      geneseqn2001bs:*
geneseqn2002bs:*
                                                                                                                                geneseqn1990s:*
geneseqn2000s:*
                                                                                                                geneseqn2001as: *
                                                                                                                                                                                                                                                            2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                      summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Search time 197.714 Seconds (without alignments) 531.011 Million cell updates/sec
                                                                                                                                                                                                                                                                                                     8269772
```

Pred. No. is the nu score greater than and is derived by s is the number of results predicted by chance to have a ater than or equal to the score of the result being printed, rived by analysis of the total score distribution.

SUMMARIES

14	2 0	) t	, a	; ;	, t	1 5	- L			<u>.</u>	10		o	· ~	ı a	٠. ٥	1 4		ر ا	. ب		NO.	Result
18.4	18.4	18.4	18.4	, L	10.4			•	18.4	18.4	18.4	ι	10.4	. 19	. 20		) N	) C	) k	) N		Score	
92.0	92.0	92.0	92.0	92.0	20.0		Ņ	•	92.0	92.0		92.0	92.0	95.0	100.0	100.0	T00.0		100.0	100.0		Match	Query
20	20	20	20	20	20	200	20	20			20		20	20	20	20	20	20	200	20		Match Length	
4.	4	4	4.	4		4	. 4	w	N	N	N	N	N	9	12	v	9	4.	L	N	:	BG	
AAF99567	AAF59504	AAC80669	AAF98731	AAF98854	AAH19262	AAH50658	AAH20394	AAA90449	AAV74245	AAV74238	AAV27654	AAV47684	AAT16894	ACA62351	AD058881	ACA62324	ACD91359	AAD02961	AAZ48834	AAV27677		ID	
		_		Aaf98854 Poly-G		Aah50658 Immu								Aca62351 Lymp	r	Aca62324 Lym;	Acd91359 B-cell	Aad02961 Imm	Aaz48834 B-cell	Aav27677 Immı		Description	
Immunosti	Immunosti	Immunogen	Human IFN	Y-G im	Oligonucl	Immune re	CpG motif	adjuv	CpG-N mot	-N mot	Immunosti	Unmethyla	Immunomod	Lymphocyt	Mitogenic	Lymphocyt	ell st	Immunosti	ell st	Immunosti			

AAV27641-751 represent immunostimulatory oligodeoxyribonucleotides (ODNs) of the invention. The ODNs contain at least one unmethylated CpG dinucleotide, and have the formula: 5 NNIXICGXZNZ 3', where at least one nucleotide separates consecutive CpGs, X1 is adenine, guanine, or thymine, X2 is cytosine or thymine, N is any nucleotide and N14NZ is 0-26 bases with the provision that N1 and N2 does not contain a CCGG tetramer or more than one CCG or CGG trimer OR 5' NX1XZCGX3X4N 3', where at least

New immunostimulatory nucleic acid molecules - which contain at least one unmethylated CpG dinucleotide, used for treating e.g. tumours, infections or autoimmune disease.

WPI; 1998-272127/24.

Disclosure; Page 25; 109pp; English.

45	44	43	. 4	41	40	ω 9	38	37	36	35	4	ü	32	31	30	29	28	27	26	25	24	23	22
18.4	18.4	٠	18.4	18.4	٠	18.4	18.4	18.4	18.4	18.4	18.4	18.4	18.4	18.4	18.4	18.4	18.4	18.4	18.4	18.4	18.4	18.4	18.4
٠	•	•	•	•	92.0	•	٠		92.0	•	92.0	92.0	٠									92.0	92.0
20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20
9	9	9	9	9	9	9	æ	œ	σ	σ	σ	0	6	Ø	9	σ	o	v	4	4	4	4	4
ADB36892	ADB37266	ADB37069	ACH03288	ACH03105	ACD99810	ACC83113	ABZ80163	ACC48308	ABS70558	AAL4488	ABK46517	ABL39033	ABL39032	ABS78035	ABS78283	ABS78485	ABS78484	AAF27750	AAS09639	AAA92361	AAF99763	AAF99390	AAF99764
Adb36892	Adb37266	Adb37069	Ach03288	Ach03105	Acd99810					Aal4488	Abk46517	Ab139033	Ab139032	Abs78035	Abs78283	Abs78485	Abs78484	Aaf27750	Aas09639	Aaa92361	Aaf99763	Aaf99390	Aaf99764
Immunosti		Immunosti	Immunosti	Immunosti	;	D class C	Immunosti	CpG oligo	Dendritic		Immunosti		Immunosti	Angiogene	Angiogene	Angiogene	Ó	P. falcip		CG motif	Immunosti	Immunosti	Immunosti

### ALIGNMENTS

RESULT 1 AAV27677 ID AAV2

AAV27677 standard; DNA; 20 BP

01-OCT-1998 (first entry)

AAV27677;

```
Krieg AM,
                                                                                                                                                              30-OCT-1996;
                                                                                                                                                                                              07-MAY-1998.
                                                                                                                                                                                                                                          Immunostimulatory; oligodeoxyribonucleotide; ODN; unmethylated CpG dinucleotide; activate; lymphocyte; immune response; Th2; Th1; cytokine; treatment; prevention; asthma; autoimmune disease; desensitisation therapy; artificial adjuvant; antibody generation; as.
                                                                                                                                                                              30-OCT-1997;
                                                                                                                                                                                                                               Synthetic.
                                                                                                                                             (IOWA ) UNIV IOWA RES FOUND.
                                                                                                                                                                                                              WO9818810-A1.
                                                                                                                                                                                                                                                                                   Immunostimulatory oligodeoxyribonucleotide of the invention
                                                                                                                              Kline JN;
                                                                                                                                                              96US-00738652
                                                                                                                                                                             97WO-US019791.
```

```
Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Regult
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB
Maximum DB
                                                                                                                                    00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OM nucleic
         a
                                                            O
           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
       Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  •
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq length: 0
seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Issued_Patents NA:*

1. /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2. /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3. /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4. /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfIles1.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  January 19, 2005, 05:57:22; Search time 48 Seconds (without alignments) 296.162 Million cell updates/sec
       IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-789-536-1
20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        824507 segs, 355394441 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ggggtcaacgttcagggggg 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
     5787
5926
5926
234
324
324
615
615
798
798
1095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BB
US-08-386-063-1
US-08-386-063-1
US-08-386-52-12
US-09-030-701-63
US-09-082-649B-52
US-09-082-649B-59
US-09-082-649B-59
US-09-082-649B-59
US-09-337-619-12
US-09-337-619-12
US-09-337-619-12
US-09-337-619-12
US-09-286-098-52
US-09-286-098-52
US-09-286-098-52
US-09-286-098-52
US-09-286-098-52
US-09-286-098-52
US-09-189-32-193A-46
US-09-288-998-2912
US-09-288-998-2912
US-09-489-039A-2912
US-09-489-039A-2912
US-09-489-039A-5251
US-09-288-998-466-386
US-09-288-998-398-585
US-09-289-991A-10728
US-09-489-039A-2753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1649014
 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
1, Appli
1, Appli
1, Appli
63, Appl
63, Appl
62, Appl
52, Appl
12, Appl
11, Appl
11, Appl
11, Appl
12, Appl
13, Appl
16, Appl
17, Appl
18, Appl
19, Appl
19,
```

음 정 포함증	US +	RESULT US-08:- US-08:- Pates Pates GENI T. T. CC	0 0000
Best Loc Matches	ATTOR NAM NEG REG REG REG REG REG REG REG REG TEL TEL TEL TEN TEN TEN TEN TOP TOP MOLEC 08-386-	ULT 1 08-386- atenice atenice atenice APPLI TITLE NUMBE CORRE CORRE CORRE CORRE CORRE CORPU SIP CONFU SIP CONFU SIP CONFU SIP CONFU SIP CONFU SIP CONFU SIP CORPE	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
1 1	CLASSIFICAN ATTORNEY/AGEN NAME: ARNA REGISTRATIC REFICENCE/I TELECOMMUNIC/ TELEPHONE: TELEPHONE: TELEPHONE: CHARTION FOR SEQUENCE CHARTION LENGTH: 20 TYPE: DIVIDIOSY: MOLECULE TYPE MOLECULE TYPE 08-386-063-1	ESULT 1 S-08-386-063-1 Sequence 1, Appli Patent No. 600820 GENERAL INFORMAT APPLICANT: AT TITLE OF INVENT NUMBER OF SEQUENT CORRESPONDENCE ADDRESSEE: 60: STREET: MOSTO, STATE: MASS, ZIP: 02109- COMPUTER READA, MEDIUM TYPE: COMPUTER READA, MEDIUM TY	11111111111111111111111111111111111111
milarity Conser 3GGTCAAC 	CLASSIFICATION: 424 TTORNEY/AGENT INFORMA NAME: ARNOLD, BETH REGISTRATION NUMBER: REPERENCE/DOCKET NUM ELECOMMUNICATION INFO TELEPHONE: (617)227-5 CORMATION FOR SEQ ID N EQUENCE CHARACTERISTI LENGTH: 20 base pai TYPE: nucleic acid GSTRANDEDINESS: singl TOPOLOGY: linear OLECULE TYPE: DNA 386-063-1	1386-063-1 1386-063-1 1ERAL INFORMATION: ERRAL INFORMATION: MPPLICANT: Arthur M. K PPLICANT: BOSTON STATE: MASSACHUSETTS COUNTRY: USA ZIP: 02109-1875 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy COMPUTER: IBM PC com OPERATING SYSTEM: PC SOFTWARE: ASCII text URRENT APPLICATION NUMBER: FILING DATE:	74.0 74.0 74.0 72.0 72.0 72.0 72.0
imilarity 100.0%; conservative 0 geogranacgrangegegegegegegegegegegegegegegegegegege	CLASSIFICATION: 424 ATTORNEY AGENT INORMATION: NAME: ANOLD, BETH E. REGISTRATION NUMBER: 35,430 REFERENCE/DOCKET NUMBER: UI TELECOMMUNICATION INFORMATION: TELEPHONE: (617)227-7400 TELEPAX: (617)227-7941 FORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 20 base pairs TYPE: nucleic acid STRANDEDMESS: single TOPOLOGY: linear MOLECULE TYPE: DNA -386-063-1	י ייט או אייט אייט אייט אייט אייט אייט א	1554 30350 50341 52297 52297 318 318 318 318 318 318 318 318 318 318
0.0*; 0.0*; e ggggg 	ION: 35, ER: 7400 7400 41 S: 1	I US/08386 I Krieg, IMMUNOMO 27 SS: 6 COCKFI 6 COCKFI 7TTS TTS TTS TTS TTS TTS TTS TTS I & COCKFI 6 COCKFI 6 COCKFI 7 COCKFI 7 COCKFI 7 COCKFI 7 COCKFI 7 COCKFI 8 COCKFI 8 COCKFI 8 COCKFI 8 COCKFI 9 CO	44183334444444444
#; Score 20; DB 3; Length 2 #; Pred. No. 0.55; 0; Mismatches 0; Indels 3GG 20 	430 UIZ-013CP I:	1 US/08386063  1. Krieg, M.D. IMMINOMODULATORY OLIGONUCLEOTIDES 27 28. 28. 27 STREET, SUITE 510  27TS  27TS  28. 29y disk 20mpatible 20cmpatible 20cmp	US-09-270-767-11891 US-10-118-328-3 US-08-247-901C-1 US-09-275-904-1 US-09-426-436-1 US-09-426-436-1 US-08-150-204E-104 US-08-150-204E-110 US-08-150-204E-110 US-08-150-204E-112 US-08-150-204E-119 US-08-150-204E-119 US-08-150-204E-119 US-08-150-204E-119 US-08-150-204E-119 US-09-489-039A-1669 US-09-489-039A-1669 US-09-539-601-4 US-10-029-907-6 US-10-029-907-7 US-10-029-907-24  ALIGNMENTS
.6 0;			Sequence Sequence
Сарв	•		11891, A 3, Appli 1, Appli 1, Appli 1, Appli 1, Appli 17, Appli 17, Appli 104, App 116, App 110, App 1110, App 1119, App 1119, App 1119, App 119, App 119, App 119, App 1106, App 1107, App 1108, App 1109, Ap

RESULT 2

0

```
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         January 19, 2005, 06:37:10 ; Search time 209.714 Seconds (without alignments) 547.973 Million cell updates/sec
                                                                                                                                                                                                                                                                   10:
11:
12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4300275 seqs, 2872944193 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-789-536-1
20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ggggtcaacgttcagggggg 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Published_Applications_NA: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
/ Cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                             / C912_6/ptodate/1/pubpna/USO6_NEW_PUB.seq:*
/C9n2_6/ptodate/1/pubpna/USO6_NEW_PUB.seq:*
/C9n2_6/ptodate/1/pubpna/USO6_NEW_PUB.seq:*
/C9n2_6/ptodate/1/pubpna/USO7_NEW_PUB.seq:*
/C9n2_6/ptodate/1/pubpna/USO7_NEW_PUB.seq:*
/C9n2_6/ptodate/1/pubpna/USO8_NEW_PUB.seq:*
/C9n2_6/ptodate/1/pubpna/USO8_NEW_PUB.seq:*
/C9n2_6/ptodate/1/pubpna/USO8_NEW_PUB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8600550
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

'n
š
ş
ᢓ
RI
SE

1110 98 76 55 4 W 2 1	No.
22222222222222222222222222222222222222	Score
100.0	Query Match Length DB
0000000000	angth D
117	B ID
US-09-415-142-1 US-09-931-583-1 US-10-631-676-1 US-10-789-051-1 US-10-789-051-1 US-10-789-536-1 US-10-789-536-1 US-10-789-353-1 US-10-789-373-1 US-10-789-199-1 US-10-789-199-1 US-10-847-650-1	0
Sequence 1, Appli Sequence 1, Appli	Description

RESULT 2 US-09-931-583-1

	44			41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13
							18.4									18.4		æ		18.4		.00	.80		8	8	8	8	8		8	8
	.~		.~	.~	.2	٠.	92.0	.~	∾	2		'n	'n		۶.				۲	Ν.	'n	'n	'n	N	ຸນ	2	'n	2	Ν	Ν	Ν	Ν
20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20
17	16	16	15	15	15	15	15	15	15	15	15	14	4	14	14	14	14	14	Ħ	11	11	Ľ	Ħ	11	10	10	10	10	10	10	10	10
-10-627-331-	-10-719-493-1	-10-455-247-	-10-314-578-96	-10-314-578-9	-10-314-578-76	-10-314-578-51	US-10-306-522-12	-10-187-264A-	-10-224-523-	-10-194-035-8	-10-161-229-47	-10-017-995-96	-10-017-995-96	-10-017-995-76	-10-017-995-51	0-112-65	-10-112-653-74	-10-112-653-49	-09-965-101-5	-965-101-52	-09-776-479-96	9-776-479-9	-09-776-479-76	-09-776-479-51	-09-967-464-3	-09-776-479-96	-776-47	-09-776-479-76	-09-776-479-51	18-918-1	9-888-326-43	9-888-326-4
equenc	equenc	equenc	eque	2	equenc	Sequence	equenc	equenc	equenc	Sequence	equenc	equenc	quenc	equenc	Sequence	Sequence	equenc	equenc	equenc	quenc	equenc	equenc	equenc	equenc	equenc	equenc	equenc	Sequence	æ	quenc	æ	Sequence
				968, App			12, Appl							- 1	7	23	2	96	٥	•	3	39	5	μ.	•	5	33	5	10	'n	ű	m

```
APPLICANT: Klinman, Dennis
APPLICANT: Klinman, Dennis
APPLICANT: Klinman, Dennis
APPLICANT: Klinman, Dennis
APPLICANT: Steinberg, Alfred D.
FILE GF INVENTION: INMINOMODULATORY OLIGONUCLEOTIDES
FILE REFERENCE: C1039/7029
CURRENT APPLICATION NUMBER: US/09/415,142
CURRENT FILING DATE: 1999-10-09
FRIOR APPLICATION NUMBER: US 08/386,063
PRIOR APPLICATION NUMBER: US 08/386,063
PRIOR FILING DATE: 1995-02-07
INUMBER OF SEQ ID NOS: 27
INUMBER OF SEQ ID NOS: 27
SEQ ID NO 1
LENGTH: 20
TYPE: DNA
OPPLANTEN: ARLIFICIAL Sequence
    밁
                                        á
                                                                                                                                                             ; ORGANISM: Artificial Sequence ; PEATURE: OTHER INFORMATION: Synthetic oligonucleotide US-09-415-142-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 1
US-09-415-142-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09415142 Publication No. US20030026782A1 GENERAL INFORMATION:
                                                                              Matches 20; Conservative
                                                                                                    Query Match
Best Local Similarity
                             1 GGGGTCAACGTTCAGGGGGG
  GGGGTCAACGTTCAGGGGGG
                                                                                               100.0%; Score 20; DB
100.0%; Pred. No. 2.3;
                                                                              0; Mismatches
20
                                    20
                                                                                                                     DB 10;
                                                                              0
                                                                                                                     Length 20;
                                                                              Indels
                                                                            0
                                                                            Gaps
                                                                            0
```

```
Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Result
No.
                                                                                                             Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
                          118.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
117.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST: 4: 95
5: 95
6: 97
7: 97
9: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32822875 seqs, 18219865908 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-789-536-1
20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              January 19, 2005, 05:49:12 ; Search time 1626.29 Seconds (without alignments) 448.134 Million cell updates/sec
                          9999tcaacgttcagggggg 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gb_est1:
gb_est2:
gb_est3:
gb_est4::
gb_est5::
gb_est6::
gb_gss1::
                          BB
                                                        BX67840

BX253784

AV294749

AV772436

CG143495

BB629098

AQ414593

BB950547

CF398170

BE643702

BB532888

AQ416817

BB5328810

BF516817

BG701308

BX6781308

BX781308

BX78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ħ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65645750
BX678404 BX678404
BX253788 BX253788
AV294749 AV294749
AV772436 AV772436
CG143495 PUIHM65TB
BB629098 BB629098
BB629098 BB629098
AQ414593 RPCI-11-1
BB629038 RPCI-11-1
BE643702 NXCI 043
BB532888 BB532888
AW888010 NXNV 105
BF516817 NXSI 003
BF516817 NXSI 003
BF716817 NXSI 003
BC701308 NXSI 062
BX678528 NXSI 062
BX678528 NXNV004A0
BC431401 NXNV 181
BQ655810 NXRV099 H
BQ702629 NXSI 130
BQ702629 NXSI 130
BQ702629 NXSI 130
BQ702629 RYDN3 B
BQ702630 RYDN3 B
BQ703680 RYDN3 RYDN3 R
B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
```

	C 45	C 44	c 43	4.	41	c 40	c 39	c 38												c 26	
	16.8	16.8	16.8	16.8	16.8	16.8	16.8	16.8	16.8	16.8	16.8	16.8	16.8	16.8	16.8	16.8	16.8	16.8			16.8
	84.0		84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0			84.0	84.0	4	84.0	84.0
	700	694	691	676	666	662	662	660	653	648	641	634	626	626	598	566	561	546	532		512
	8	7	7	7	7	7	7	7	v	7	υ	თ	_	۲	7	7	7	۳	4.	σ	N
	AQ888815	CO174200	CF473420	CF670509	CO199154	CF390498	CF386290	CF401770	BQ633853	CF389798	BX784262	BX253042	AA557077	AL751023	CF392026	CF476621	CF673102	AA556997	BG275515	CA354197	BF517774
•		0	_			_	O RTDR1	_	NXRV061		BX784262 BX784262	BX25		AL7510	CF392026 RTDR3_12	RTWW3	RTCN	7 839 Ī		CA354197 625871 NC	w

# ALIGNMENTS

	ORIGIN
/organism="Pinus pinaster"	
1. 414	source
Location/Qualifiers	FEATURES
route d'Arcachon 33612 Cestas CEDEX France Email: Frigeriospierroton.inra.fr Email: Frigeriospierroton.inra.fr Seq primer: T3.	
Genetique et Amelioration 69	
Contact: Frigerio JM	JOURNAL COMMENT
Identification of water-deficit responsive genes in Maritime pine	TITLE
Frigerio, J. and Plomion, C.	AUTHORS
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. 1 (bases 1 to 414)	REFERENCE
Pinus pinaster	ORGANISM
EST. Pinus pinaster	SOURCE
BX678404.1 GI:38012342	VERSION
BX678404 KS FINUS PINASCER CUNA CIONE RSUBFU9, mRNA sequence.	ACCESSION
414 bp	Locus
	BX678404/C

Query Match
Best Local Similarity
Matches 19; Conserv

Conservative

92.0%;

Score 18.4; DB 5; Pred. No. 1.4e+02; 0; Mismatches 1;

Length 414; Indels

<u>.</u>

Gaps

0

```
Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                      Database :
                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Run on:
GenEmbl:*
1: gb ba:*
2: gb htg:*
3: gb intg:*
3: gb om:*
5: gb ow:*
6: gb pat:*
6: gb pat:*
7: gb ph:*
9: gb pr:*
9: gb pr:*
10: gb ro:*
11: gb ste:*
12: gb sy:*
13: gb un:*
14: gb vi:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                 IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           January 19, 2005, 01:27:37 ; Search time 441 Seconds (without alignments) 1608.493 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                            4526729 seqs, 23644849745 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-789-536-6
15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 gcatgacgttgagct 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                 9053458
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1.7	1 0	18	17	-	1 5	7.		13	12	-	: 5	<b>.</b>	٥	<b>a</b>		<b>.</b> .	ית	ъ	4		J ;	J	_	No.	Result
T-3	i ,	<u>,</u>	15	Ţ	: 5	. i	7	15	15	15	Ĺ	, ,	7	15	7.5	, <sub>L</sub>	7 1	15	15			,	15	Score	
T00.0		2	100.0	T00.0	100.0	9 6	100	100.0	100.0	100.0	100.0		000	100.0	100.0		200	100.0	100.0	100.0		3	100.0	Match	Query
77		ń	-5	15	1	• •	1 1	7	15	15	15	. L	1	15	15	Ļ	1	, ,	15	15		4 1	15	Match Length	
o	٠, ٥	٠,	v	0	σ	٠, ٥	١ (	ת	σ	თ	6	0	١,	σ	0	σ	١.	'n	σ	0	σ	١,	ע	88	
AR432429	AR444180	10000	AR213813	BD270732	BD267861	BD26/831	000000000000000000000000000000000000000	BD361336	BD261093	BD261057	BD205551	BU205515	100000000000000000000000000000000000000	AR154677	AR146329	AK146293	1010A	20140400	AR140457	AR140447	AK135035	*****	AROGAGOI	ID	
			-																						
AR432429	AR222180	TELEGIST	7011011	BD270732	BD267861	BD267831	977747A		BD361093	BD261057	BD205551	BD205515	// OFCT NW	201675	AR146329	AR146293	AKI40489	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	AR140457	AR140447	AR135035	TEGGEORY	200000	Description	
Sequence	Sequence	sequence		Stereoiso	Methods f	Methods f	Methods a	מופרווטעס מ			Method of	Method of	Sequence	20000	Segmence	Sequence	Sequence	DOMESTIC OF	Semience	Sequence	Sequence	sequence		ion	

								_																
4.5	44	. 4	4.2	e	4 6		8 6	C 37	16			. u	) L	31	30	2	28	27	26	25	C 24	23	22	2
15	15	15	15	5	5	5	15	15	15	5	15	5	15	15	15	ŭ	15	15	15	15	15	5	15	5
100.	100.0	100.0	100.	٠	100.	٠	•					100.0	100.	100.0	100.	100.	100.	100.0	100.0	100.0	•	100.0	100.	TOO.
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		c
15	15	15	15	5	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	ŗ
σ	σ	6	0	σ	σ	σ	σ	6	σ	6	σ	σ	9	o	0	9	6	σ	σ	σ	δ	0	6	σ
AX54	AX54	AX54	AX45	AX35	AX35	AX35	AX35	AX35	AX35213	AX35	AX35189	AX35	AX35	AX3	AX3	AX3	AX3	AX3	AX34238	AX1	X 1X 1	AX1	AX1	AXI
AX547627	AX546947	AX546927	AX455576	AX355294	AX355293	AX355292	AX355291	AX355037	2131	AX352112	1892	AX351871	AX351844	AX351820	AX351799	AX351733	AX342443	AX342410	12383	AX105164	AX104643	AX104591	AX104574	AXIO3894
ķ	Æ	Æ	Ž	ğ	A.	Ą	¥	\$	Ž	ž	A.	⋧	₹	Æ	\$	\$	ž	¥	₹	2	₹	Ž	Ş	Ž
AX547627	AX546947	<b>AX546927</b>	AX455576	1X355294	AX355293	AX355292	<b>1</b> 355291	AX355037	AX352131	AX352112	AX351892	AX351871	AX351844	1X351820	AX351799	AX351733	AX342443	AX342410	AX342383	AX105164	AX104643	AX104591	AX104574	AX103894
Seq.	Seg	Seq	Seg	Seg	Seg		Seg	Seg	Seq	Seg	Seq	Seg	Seg								Sec	Sec	Sec	
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequenc	Sequence	Sequence	Sequence	Sequence	Sequenc	Sequenc	Sequenc	Sequenc

RESULT 2 AR135035 LOCUS LOCUS DEFINITION SA ACCESSION AF VERSION AF VERSION AF COMPACE UT REFERENCE 1 AUTHORS Kx TITLE IT	Query Match Best Local Similarity Matches 15; Conser  Qy 1 GCATGACGTT                     Db 1 GCATGACGTT	RESULT 1 AROS6691 LOCUS DEFINITION S ACCESSION A VERSION A VERSION A KEYWORDS SOURCE ORGANISM U REFERENCE 1 AUTHORS TITLE JOURNAL P FEATURES BOUTCE ORGIN
AR135035 Sequence 6 from patent US 6194388. AR135035 AR135035.1 GI:14123940 Unknown. Unknown. Unclassified. 1 (bases 1 to 15) Krieg,A.M., Klinman,D. and Steinberg,A.D. Immunomodulatory oligonucleotides	100.0%; Score 15; DB 6; imilarity 100.0%; Pred. No. 9.1e+02; Conservative 0; Mismatches 0; GCATGACGTTGAGCT 15	AR096691 AR096691 AR096691 AR096691.1 GI:10025709  . Unknown. Unknown. Unclassified. 1 (bases 1 to 15) Krieg, A.M. Immunomodulatory oligonucleotides Patent: US 6008200-A 6 28-DEC-1999; Location/Qualifiers 1. 15 1. 15 1. 15 /mol_type="unassigned DNA"
linear	, Length 15; 02; 0; Indels	linear
PAT	0,	PAT
16-MAY-2001	Gaps 0;	08-SEP-2000

```
Minimum
Maximum
                                                                                                                                                                                                                Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title:
Perfect score:
                                                                                                                                                                                                                                                                               Post-processing:
                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OM nucleic -
                                                                                                                                                                                                                                                                                                             DB seq length: 0
DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                  4134886 seqs, 2624710521 residues
                                                                                                                                                                       N_Geneseq_23Sep04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
                                                                                                                                                                                                                                                             Minimum Match 0%
Maximum Match 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-789-536-6
15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         January 19, 2005, 01:18:22;
                                                                                                                                                                                                                                             Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gcatgacgttgagct 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.
                                                     geneseqn2002bs:*
geneseqn2003as:*
geneseqn2003bs:*
                                                                                                        geneseqn2002as:*
                                                                                                                          geneseqn2001bs:*
                                                                                                                                          geneseqn2001as:*
                                                                                                                                                          geneseqn2000s:
geneseqn2003cs:*
geneseqn2003ds:*
geneseqn2004s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Search time 148.286 Seconds (without alignments) 531.011 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                  8269772
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

2
¥
3
55
H
ò

2	2 6	) <del> </del>		<u> </u>	1 6		· .	. L	. L	÷ +	: 5		9 0	o <b>~</b>	Jo	n (	n 4	٠ (	, د	J	-	No.	Result
15	. L				, t	: L		. 15	15			1 1	, ,	, L		1 6	, L	, t	1 1	10	15	Score	
100.0	T00.0	100.0	100.0	T00.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0									200	100.0	Match	Ouerv
15	15	15	15	15	15	15	15	15	15	15	1	1 5	. L	15	1 5	: 5		L		,		Match Length	
4	4.	4	4	4	4	4.	W	w	w	w				N	N	١,	۸ (	ν.	۸ (	) !		BG	
AAH78645	AAD02966	AAF98790	AAH19298	AAH19266	AAH19256	AAH50576	AAZ47606	AAZ47628	AAZ48839	AAZ47812	AAZ47963	AAZ47936	AAZ60937	AAZ41887	AA241860	AAV27712	AAV27679	AAV27673	AAV27727		PAVEDEE	ID	
		. Aaf98790 CpG immun	. Aah19298 Oligonucl	Aah19266 CpG Oligo	Aah19256 Phosphoro			Parasi		Immunos	Aaz47963 Immune re	Aaz47936 Immune re	Aaz60937 Nucleotid	Aaz41887 IL-12 sec	Aaz41860 IL-12 sec	Aav27712 Immunosti	Aav27679 Immunosti	Aav27673 Immunosti	Aav27727 Immunosti	May52553 Unmernyla		Description	

...

a	0		n
4443	38 40 410	0 0 1 2 8 8 8 8 7 8 7 8 8 8 8 8 8 8 8 8 8 8 8	222222
15 15 15	15 15 15	15 15 15 15 15 15 15	15 15 15 15 15 15 15
100.0	100.0	100.0 100.0 100.0 100.0 100.0	100.0 100.0 100.0 100.0 100.0
15 15 15	15	15 15 15 15 15 15 15 15 15 15 15 15	15 15 15 15 15
0000	0000	<b>ຓຓຓຓຓຓຓຓ</b> ຓ	44440
ABL38702 ABL38923 ABL38921 ABL38920	ABS77602 ABS78351 ABS78282 ABL38922	ABLJ35186 ABLJ35186 ABLJ35502 ABLJ35205 ABLJ52252 ABLJ52271 ABS77582 ABS77829	AAF99583 AAF99566 AAF99630 AAF98941 AAF98961 AAF78474 ABL35122
Abl38702 Abl38923 Abl38921 Abl38920	Abs77602 Abs77602 Abs78351 Abs78282 Ab138922	Abl35485 Abl35186 Abl35505 Abl35205 Abl35252 Abl35252 Abl35271 Abl35271 Abs787968	Aaf99583 Aaf99566 Aaf99630 Aaf98941 Aaf98961 Aah78474 Abl35122
Immunosti Immunosti Immunosti	Angiogene Angiogene Angiogene Angiogene Immunosti	Immunosti Angiogene	Immunosti Immunosti Immunosti Immunosti Immunosti Nucleotid Immunosti

# ALIGNMENTS

RESULT 1 AAV52553 Unmethylated CpG dinucleotide; immune response; bacterial meningitis; natural killer cell activation; NK cell; Th2 response; neonatal sepsis; pulmonary disorder; asthma; environmentally induced airway disease; bacterial infection; endotoxaemia; therapy; cystic fibrosis; inflammatory bowel disease; ss. 28-FEB-1997; 25-FEB-1998; 03-SEP-1998. WO9837919-A1. Synthetic. Unmethylated CpG dinucleotide 1823. AAV52553; AAV\$2553 standard; DNA; 15 BP (IOWA ) UNIV IOWA RES FOUND. 20-NOV-1998 (first entry) 97US-0039405P. 98WO-US003678

Use of nucleic acids containing an unmethylated CpG - f subject having or at risk of having an acute decrement inhibiting an inflammatory response. for treating a t in air flow or

WPI; 1998-480941/41. Schwartz DA, Krieg

A M

Example 4; Page 35; 65pp; English.

This sequence represents an unmethylated CpG dinucleotide, and can be used in the method of the invention. The method is for treating a subject having, or at risk of having an acute decrement in air flow, comprising administering a nucleic acid sequence containing at least one unmethylated CpG. The nucleic acids containing an unmethylated CpG dinucleotide affect an immune response in a subject by activating natural

```
Regult
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Run
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92:
                     225
225
235
24
25
25
26
26
26
27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
                seq length: 0
seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
Match Length
             100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
100.00
10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IBsued_Patents_NA:*

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-789-536-6
15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                January 19, 2005, 05:57:22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    824507 seqs, 355394441 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gcatgacgttgagct 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
             519
999
11001
11001
11842
11842
12955
3039
3808
3808
3808
3808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BB
     US-08-386-063-6
US-08-386-063-6
US-08-38-652-16
US-08-738-652-18
US-08-738-652-48
US-09-286-098-5
US-09-286-098-5
US-09-286-098-5
US-09-325-193A-5
US-09-325-193A-5
US-09-325-193A-5
US-09-325-193A-5
US-09-325-193A-154
US-09-337-619-6
US-09-343-681A-154
US-09-543-681A-159
US-09-489-039A-90
US-09-481-638-261
US-09-481-638-261
US-09-481-638-261
US-09-543-681A-1840
US-09-543-681A-1840
US-09-620-312D-675
US-09-620-312D-675
US-08-972-631-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Search time 36 Seconds (without alignments)
296.162 Million cell updates/sec
Sequence 6, Appli
Sequence 6, Appli
Sequence 16, Appli
Sequence 18, Appli
Sequence 35, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 1544, Appli
Sequence 1544, Appli
Sequence 1544, Appli
Sequence 261, Appli
Sequence 31, Appli
Sequence 361, Appli
Sequence 361, Appli
Sequence 31, Appli
Sequence 33, Appli
Sequence 33, Appli
Sequence 31, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
     RESULT 2
```

0000000

용 성	3 m O	US-					** ** ** *		RES US-	n	n	0 0 0	0
	Query Ma Best Loc Matches	INFORMATION SEQUENCE ( LENGTH: TYPE: ITYPE: TYPE: TYPE: TYPE: TYPOLOGI MOLECULE 1 08-386-063-0	ATTOI NAN REC TELEC	SOI CURRI API	COMPUTER MEDIUM COMPUTI	081	CORRI	Patent No GENERAL APPLIC TITLE NUMBER	ULT 1 08-386	4 4 4 4 5 4 4 2	2 C C C C C C C C C C C C C C C C C C C		2098
1 GCA 1       1 GCA	Match Local Sim es 15;	ORMATION FOR S EQUENCE CHARAC LENGTH: 15 b TYPE: nuclei STRANDEDNESS: TOPOLOGY: 11 OLECULE TYPE: 386-063-6	CLASSIFICATION: CLASSIFICATION: ATTORNEY/AGENT IN NAME: ARNOLD, REGISTRATION NU REFERENCE/DOCKE TELECOMMUNICATION TELECOMMUNICATION TELECOMMUNICATION TELECOMMUNICATION TELECOMMUNICATION TELECOMMUNICATION TELECOMMUNICATION	SOFTWARE: ASCII te CURRENT APPLICATION D APPLICATION NUMBER:	MPUTER REMEDIUM TY MEDIUM TY COMPUTER: COMPUTER:	TRY:	CORRESPONDENCE ADDRESSEE: STREET: 60		၈ရို	11 11 11 11 11 11 11 11 11 11 11 11 11		13.4 13 13	
GCATGACGTTGAGCT             CATGACGTTGAGCT	Similarity 5; Conserva	FOR SEQ 1: HARACTERII 15 base   ucleic ac NESS: si : linear YPE: DNA	ICATION: ICATION: AGENT INF ARNOLD, B ARTION NUM CE/DOCKET NICATION NE: (617)	ASCII LICATIO ON NUMB	ADABI PE:	MASSACHUSETTS		OF SECUENCE	plication	0000	86.7 86.7 86.7	, , , , , , , , ,	999
TGAGCT	100. 100. vative	of FOR SEQ ID NO: CHARACTERISTICS: 15 base pairs nucleic acid DNESS: single Y: linear TYPE: DNA	ATI E. MBE	DAT	FORM:	JSETTS	STR STR	. z		444	1551 1551 1551 2046 2085	111282 343 528 1089 1179	4748 6045 10320
15 15	0 0 * *		ON: 35, 35, ATIO	\$/0	disk		COCKF	ieg	083	τυ 4 <b>.</b> ω ω	140041		444
	; Score 15; DB 3; Length ; Pred. No. 9.6; 0; Mismatches 0; Indel	<del>.</del>	; ,430 UIZ-013CP ION:	/08/386,063	disk - DOS/MS-DOS		FIELD SUITE 510	Krieg, M.D. IMMUNOMODULATORY OLIGONUCLEOTIDES	ALIGNMENTS US/08386063	PCT-US95-05758-29 US-09-634-238-131 US-09-103-840A-2 US-09-103-840A-2	457-274A-1 457-274A-2 95-05758-1 95-05758-2 95-039A-4 457-274A-2	US-09-754-250-3 US-08-349-403-7 US-09-248-796A-3977 US-09-489-039A-2302 US-09-602-787A-185	0000
	15						•	02		0 00 0 0 00 00		00000	0 0 0 0 0 0 0
	0,									Sequence Sequence Sequence Sequence	sequence sequence sequence sequence sequence sequence	Sequence Sequence Sequence Sequence	equence equence
	Gaps	·		,						131,	1, 1 1, 1 27, 27, 469; 29,	180	
	0,									F F 0 P	-0	-0-0-0 P-P	- 1- 1-

```
Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Perfect score:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-789-536-6
15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          January 19, 2005, 06:37:10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4300275 seqs, 2872944193 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 gcatgacgttgagct 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                           /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US09NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cgn2_6/ptodata/1/pubpna/PCT_NEW PUB.seq:*
/cgn2_6/ptodata/1/pubpna/USO6_NEW PUB.seq:*
/cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/USO7_NEW PUB.seq:*
/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/USO8_NEW PUB.seq:*
/cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /pubpna/US07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Search time 157.286 Seconds (without alignments) 547.973 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PUBCOMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8600550
```

3	
₹	
3	
2	
2	

12	11	10	9	8	c 7	6	ហ	4	u	N		Result No.
15	15	15	15	15	15	15	15	15	15	15	15	Score
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	Query
15	15	15	15	15	15	15	15	15	15	15	15	Length
10	10	10	10	10	10	10	9	9	9	9	9	DB
US-09-818-918-6	US-09-888-326-322	US-09-888-326-321	US-09-888-326-320	US-09-888-326-319	US-09-888-326-65	US-09-415-142-6	US-09-920-313-5	US-09-895-007A-5	US-09-800-266A-5	US-09-824-468-41	US-09-824-468-5	ID
Sequence 6, Appli	Sequence 322, App	Sequence 321, App		319,	•	Sequence 6, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 5, Appli	•	-	Description

RESULT 2

C 33333333333333333333333333333333333	C 222 222 222 222 222 222 222 222 222 2	13 14 15 16 17 18 19 0
15 100.0 15 100.0 15 100.0 15 100.0 15 100.0 15 100.0 15 100.0 15 100.0		15 100.0 15 100.0 15 100.0 15 100.0 15 100.0 15 100.0 15 100.0
<b>ហែលសំហេសសំហេសសំហេស</b>	;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;	
US-10-023-909A-5 US-10-112-653-80 US-10-112-653-83 US-10-112-653-756 US-10-112-653-756 US-10-112-653-756 US-10-017-995-86 US-10-017-995-86 US-10-017-995-766 US-10-017-995-766	-09-954-9878 -09-874-991C -09-874-991C -09-874-991C -09-874-991C -09-874-991C -09-874-991C -09-874-991C -09-776-479-8	-09-818-918-16 -09-818-918-48 -09-931-583-6 -09-776-479-66 -09-776-479-76 -09-776-479-78
Sequence Sequence Sequence Sequence Sequence Sequence G G Sequence G Sequence G Sequence	7 8 8 7 7	
100 65, Appl 1 100 80, Appl 1 100 80, Appl 1 100 80, Appl 100 8756, Appl 100 86, Ap	9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	e e e e e e e e e e e e e e e e e e e

```
Sequence 5, Application US/09824468
Patent No. US20020064515A1

GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
APPLICANT: Weiner, George
TITLE OF INVENTION: Methods and Products for INVENTION: Immune System Using Immune TITLE OF INVENTION: Cytokines
TITLE OF INVENTION: Methods and Products for
TITLE OF INVENTION: Meth
밁
                                                                                  S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 1
US-09-824-468-5
                                                                                                                                                                                                                                                                                                                                                                                                  US-09-824-468-5
                                                                                                                                                                                                                                       Query Match
Best Local S
                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
OTHER INFORMATION: Synthetic Sequence
                                                                                                                                                                                         y Match 100.0%;
Local Similarity 100.0%;
hes 15; Conservative 0
                                              GCATGACGTTGAGCT 15
GCATGACGTTGAGCT 15
                                                                                                                                                                                              0,
                                                                                                                                                                                         Score 15; DB 9; Pred. No. 1.7e+02; D; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for Stimulating the Immunotherapeutic Oligonucleotides and
                                                                                                                                                                                                                                                                                      Length 15;
                                                                                                                                                                                              Indels
                                                                                                                                                                                              <u>,,</u>
                                                                                                                                                                                              Gaps
                                                                                                                                                                                              ç
```

```
Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum
Maximum
                                                                                                                                                                                                                                                                                                                                                                                                                           Database :
                         000000000000000
                                                                                                                                                                      Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Run
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OM nucleic -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9::
                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic search, using sw model
     100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
                                                                                                                                                                                                                                                Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32822875 seqs, 18219865908 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     January 19, 2005, 05:49:12 ; Search time 1219.71 Seconds (without alignments)
448.134 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-789-536-6
15
                                                                                                                                                                                                                                                                                                                                                                                                                                            Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gcatgacgttgagct 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                     gb_est1: *
gb_est2: *
gb_htc: *
gb_est3: *
gb_est5: *
gb_est5: *
gb_est6: *
gb_gs81: *
      명
                                                                                                                                                            AJ494293
AJ494293
AJ494285
AW145624
BW242018
BP094747
              AV985099
BU655032
                                                                                                                     AV988927
AV948910
AV984785
                                                    BW339646
                                                                                                                                                  AJ495145
                                                                                                                                                                                                                                                                            SUMMARIES
                                     AA437702 ve32g12.r
AJ494292 AJ494293
AJ494293 AJ494293
AJ494285 AJ494291
AJ494285 AJ494291
AJ494285 AJ4942018
BP094747 BP094747
AJ495145 AJ495145
AV988927 AV988927
AV948910 AV948910
AV994785 AV984785
AV996055 AV996055
BW35363 BW35363
BW345567 BW345567
BW3452814 BW352814
BW244380 BW244959
BW344959 BW244959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65645750
                                                                                                                                                                                                                BW247469 BW247469
AA437702 ve32g12.r
                                                                                                                                                                                                                                              Description
RESULT 2
AA437702/c
LOCUS
                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                             SOURCE
ORGANISM
                                                밁
                                                                  Ś
                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
VERSION
KEYWORDS
                                                                                                                            ORIGIN
                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                            COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 1
BW247469/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                Bource
AA437702
```

																•				
۸.				n				Ω 											0	
ŭ	4	ü	N	-	40	9	8	37	6	ü	4	u	32	31	8	29	28	27	26	25
15	15	2	5	15	15	5	5	15	5	15	15	5	5	15	5	15	15	5	5	15
100	100	100	100	100	100.0	100	100	100	100	100	100	100	100	100	100	100	100	100	100.	100
71	70	70	70	69	682	67	67	5	5	66	66	613	63	65	6.	64	64	64	59	64
					5															ω 
																				51 E
W12	W43	W26	W24	V97	3W23	11M	¥35	66A	3W43	3W43	3065	3W25	<b>V67</b>	3W24	1467	3W25	66A\	3W34	86A\	3W43
BW124438	BW431183	BW268555	BW243655	AV974313	BW230554	BW113437	CA350833	AV990599	BW434636	BW433399	BU655036	BW254503	AV672377	BW244852	AV672198	BW259692	AV996231	BW347242	AV988282	BW434148
_	_	•	٠.	_	_	_	_	_	٠,	u	01	_	7	١٠٠	w	.~	-	.~	٠	w
1MB	BW4	BW2	BW2	AV9	BW2	BW1	S	AV9	BW4	BW4	BU6	BW2	AV6	BW2	AV6	BW2	AV9	BW3	AV9	BW4
BW124438	BW43118	BW26855	BW24365	AV97431	BW230554	BW113437	CA350833	AV990599	BW434636	BW433399	BU655036	BW254503	AV672377	BW244852	AV672198	BW259692	AV996231	BW347242	AV988282	BW434148
_	ω	5	5	ω								-								
BW12443	BW43118	BW26855	BW24365	AV97431	BW23055	BW113437	621736	AV990599	BW43463	BW43339	1112117	BW25450	AV67237	BW24485	AV67219	BW25969	AV99623	BW347242	AV988282	BW43414
443	118	8555	365	431	550	343	36 -	959	4636	339	117	450	237	485	219	969	623	724	828	414
۳	_	٠.	ທ	_		7	กี	J	·	w	בַ	w	7	N	ω	N	_	N	N	8

ALIGNMENTS

Query Match 100.0%; Best Local Similarity 100.0%; Matches 15; Conservative 0; 1 (bases 1 to 153)
Satou, Y., Shin-i, T., Kohara, Y. and Satoh, N.
Expressed genes in Ciona intestinalis (2002c)
Unpublished (2002)
Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-705-1113
Fax: 81-75-705-1113 1 GCATGACGTTGAGCT 15 BW247469

153 bp mRNA linear EST 09-NOV-2002

BW247469 Nori Satoh unpublished cDNA library, tailbud embryo Ciona

intestinalis cDNA clone citb074008 5', mRNA sequence. Ciona intestinalis Ciona intestinalis Email: satch@ascidian.zool.kyoto-u.ac.jp. Bukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Cionidae; Ciona. BW247469.1 GI:24827387 GCATGACGTTGAGCT /tissue\_type="whole animal" /dev\_stage="tailbud embryo" /clone\_llb="Nori Satoh unpublished cDNA library, tailbud embryo" /organism="Ciona intestinalis" /mol type="mRNA" /db xref="taxon:7719" /clone="citb074008" Location/Qualifiers 48 o, Score 15; DB 5; Pred. No. 9e+02; Mismatches DB 5; Length 153; 0 Indels <u>,</u> Gaps 0

355

ģ

mRNA

linear

EST 30-MAY-1997